Amendments to the Specification:

Please replace the paragraph beginning at page 9, line 27, with the following amended paragraph:

In one aspect, the invention encompasses a peptide library comprising a collection of structurally constrained peptides. Each peptide member of the library comprises amino acid sequence C1-A1-A2-$(A3)_n$-A4-A5-C2 (SEQ ID NO:1), wherein

A1, A2, A3, A4, and A5 are naturally occurring L-amino acids;

the ~~carboxy-~~amino terminus of Cysteine C1 is optionally protected with ~~carboxy-~~an amino protecting group;

the ~~amino~~ carboxy terminus of Cysteine C2 is optionally protected with ~~an amino~~ carboxy protecting group;

A1 and A5 are selected from the group consisting of amino acids W,Y, F, H, I , V and T;

Please replace the paragraph beginning at page 10, line 16 with the following rewritten paragraph:

In the peptides of the invention, the number of the A3 residues n can be 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12; preferably 4, 5, 6, 7, 8, 9, or 10; and more preferably 4, 5, or 6. In one embodiment, n is 4 and the resulting peptides are decamers. In these decamers, the residue sites A1, A2, A4 and A5 are each from a selected group of amino acid residues as described above, whereas the middle $(A3)_4$ is a tetrapeptide sequence with varying amino acids. In one aspect of the invention, the $(A3)_4$ tetrapeptide sequence is selected from those favorable to forming a β-turn structure, including but not limited to EGNK [SEQ ID NO: 44], ENGK [SEQ ID NO: 45], QGSF [SEQ ID NO: 46], VWQL [SEQ ID NO: 47], and GPLT [SEQ ID NO: 48].

Please replace the paragraph beginning at page 10, line 30 with the following amended paragraph:

The carboxy terminal end and the amino terminal end of the cyclic peptide may be protected with any known protecting groups or may be bonded to other amino acid residues (generally naturally occurring residues), both in the (L) and in the (D) form through conventional amide peptide bonds. One embodiment of the present invention comprises the peptide X_n-C1-A1-A2- $(A3)_n$-A4-A5-C2-X_n, wherein C1 and C2 are cysteines; A1, A2, A3, A4, and A5 are

naturally occurring L-amino acids; A1 and A5 are independently amino acids W, Y, F, H, I, V, or T; A2 and A4 are independently amino acid W; A3 is any naturally occurring L-amino acid and n is an integer that is 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12; X consists of any naturally occurring amino acid and n is any integer from 1 to about 50; and C1 and C2 together form a disulfide bond thereby forming a cyclic peptide; the amino terminus of C1 is optionally protected with an amino protecting group; and the carboxy terminus of C2 is optionally protected with a carboxy protecting group [SEQ ID NO: 49]. The protecting groups and additional residues can be added using conventional peptide synthesis techniques. Generally from 1 to about 50, preferably from 1 to about 20, amino acid residues may be present on each of the carboxy and amino terminal positions, independently. These additional residues may be part of a known protein containing a beta turn of interest or may be any other desired sequence of residues. These additional residues may be added to determine the effect of the beta turn structure on the structure of the overall polypeptide or to determine the effect of the additional residues on the binding of the beta turn cyclic peptide with a protein of interest.

Please replace the paragraph beginning at page 12, line 26, with the following rewritten paragraph:

A 16-mer peptide derived from the protein ubiquitin but with a statistically more common turn sequence (MQIGVKNPDGTITLEV (SEQ ID NO: 41)) did form a highly populated hairpin in water (ca. 80%). but the hairpin did not have the same strand register as in the native protein (Searle *et al.* (1995) *Nat. Struct. Biol.* 2:999-1006). Another group studied a similar peptide in which the turn region was replaced with several sequences (MQIGVKSXXKTITLKV (SEQ ID NO: 42)), wherein XX = pro-ala or pro-gly; Haque & Gellman (1997) *J. Am. Chem. Soc.* 119:2303-2304). Evidence for the hairpin structure, with native strand register, was observed for turns containing D-amino acids but not for L-amino acid sequences. No population estimates were given in this study.